1600

RAW SEQUENCE LISTING   DATE: 07/16/2003
PATENT APPLICATION: US/10/017,479A   TIME: 15:45:40

         Input Set : A:\13407-012001.txt
         Output Set: N:\CRF4\07152003\J017479A.raw

 4 <110> APPLICANT: Reenan, Robert A.
 5   Rogina, Blanka
 6   Helfand, Stephen L.
 9 <120> TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING CELLULAR
10   TRANSPORTERS AND METHODS OF USE THEREOF
13 <130> FILE REFERENCE: 13407-012001
15 <140> CURRENT APPLICATION NUMBER: US 10/017,479A
16 <141> CURRENT FILING DATE: 2001-12-12
18 <150> PRIOR APPLICATION NUMBER: US 60/255,013
19 <151> PRIOR FILING DATE: 2000-12-12
21 <160> NUMBER OF SEQ ID NOS: 6
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1719
27 <212> TYPE: DNA
28 <213> ORGANISM: Drosophila melanogaster
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)...(1716)
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35 atg gaa att gaa att ggc gaa caa ccc cag cct ccg gtg aag tgc tcc   48
36 Met Glu Ile Glu Ile Gly Glu Gln Pro Gln Pro Pro Val Lys Cys Ser
37 1   5   10   15
39 aac ttc ttc gct aac cac tgg aag gga ttg gtt gtg ttc ctg gtg ccg   96
40 Asn Phe Phe Ala Asn His Trp Lys Gly Leu Val Val Phe Leu Val Pro
41   20   25   30
43 ctg cta tgt ctg cct gtt atg ctg cta aac gaa ggc gcc gaa ttt cgg   144
44 Leu Leu Cys Leu Pro Val Met Leu Leu Asn Glu Gly Ala Glu Phe Arg
45   35   40   45
47 tgc atg tac ctc ctt ttg gta atg gcc ata ttt tgg gtt acg gaa gcc   192
48 Cys Met Tyr Leu Leu Leu Val Met Ala Ile Phe Trp Val Thr Glu Ala
49   50   55   60
51 ttg cct ctc tat gtg acg tcc atg ata ccg att gtg gcc ttc cca ata   240
52 Leu Pro Leu Tyr Val Thr Ser Met Ile Pro Ile Val Ala Phe Pro Ile
53 65   70   75   80
55 atg ggt ata atg agc tcg gat cag act tgc cgc ttg tac ttc aag gat   288
56 Met Gly Ile Met Ser Ser Asp Gln Thr Cys Arg Leu Tyr Phe Lys Asp
57   85   90   95
59 acg ctg gtg atg ttc atg ggc ggc att atg gtc gcc ctg gct gtg gag   336
60 Thr Leu Val Met Phe Met Gly Gly Ile Met Val Ala Leu Ala Val Glu
61   100   105   110
63 tac tgt aat cta cac aaa cgt ctt gcc ttg agg gta atc cag atc gtg   384
64 Tyr Cys Asn Leu His Lys Arg Leu Ala Leu Arg Val Ile Gln Ile Val

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65          115                120                125
67 ggc tgc agt ccc cgc aga tta cac ttt ggc ctc atc atg gtt aca atg      432
68 Gly Cys Ser Pro Arg Arg Leu His Phe Gly Leu Ile Met Val Thr Met
69     130                135                140
71 ttt ttg agc atg tgg att tcg aac gcc gcc tgt act gcc atg atg tgt      480
72 Phe Leu Ser Met Trp Ile Ser Asn Ala Ala Cys Thr Ala Met Met Cys
73 145                150                155                160
75 ccg att atc caa gcc gtg ctg gag gag ctg cag gct cag ggt gtc tgc      528
76 Pro Ile Ile Gln Ala Val Leu Glu Glu Leu Gln Ala Gln Gly Val Cys
77                165                170          175
79 aaa atc aac cat gag cct caa tac caa atc gtt gga ggc aac aag aaa      576
80 Lys Ile Asn His Glu Pro Gln Tyr Gln Ile Val Gly Gly Asn Lys Lys
81             180                185                190
83 aac aac gag gat gag cca cca tac ccc acc aag atc act ctg tgc tac      624
84 Asn Asn Glu Asp Glu Pro Pro Tyr Pro Thr Lys Ile Thr Leu Cys Tyr
85          195                200                205
87 tat ctg ggc att gcc tac gcc tcc tcg ctg ggt ggc tgt gga acc atc      672
88 Tyr Leu Gly Ile Ala Tyr Ala Ser Ser Leu Gly Gly Cys Gly Thr Ile
89     210                215                220
91 atc gga act gcc acc aat ctt acc ttc aag ggc atc tac gag gct cgt      720
92 Ile Gly Thr Ala Thr Asn Leu Thr Phe Lys Gly Ile Tyr Glu Ala Arg
93 225                230                235                240
95 ttc aag aac tcc acc gaa cag atg gac ttc ccc acc ttc atg ttc tac      768
96 Phe Lys Asn Ser Thr Glu Gln Met Asp Phe Pro Thr Phe Met Phe Tyr
97                245                250                255
99 tcg gtg cca tcc atg ttg gtc tac acc ttg ctg aca ttc gtg ttc ctg      816
100 Ser Val Pro Ser Met Leu Val Tyr Thr Leu Leu Thr Phe Val Phe Leu
101             260                265                270
103 caa tgg cac ttc atg ggt ctg tgg cgt ccc aag agc aag gag gca cag     864
104 Gln Trp His Phe Met Gly Leu Trp Arg Pro Lys Ser Lys Glu Ala Gln
105          275                280                285
107 gaa gtc cag agg gga cga gag ggc gcc gat gtc gcc aaa aag gtt atc     912
108 Glu Val Gln Arg Gly Arg Glu Gly Ala Asp Val Ala Lys Lys Val Ile
109     290                295                300
111 gat cag cgc tac aag gat ctg ggt ccc atg tcc att cac gag atc caa     960
112 Asp Gln Arg Tyr Lys Asp Leu Gly Pro Met Ser Ile His Glu Ile Gln
113 305                310                315                320
115 gtg atg att ctg ttc att ttt atg gtt gtg atg tac ttc acc cgc aag     1008
116 Val Met Ile Leu Phe Ile Phe Met Val Val Met Tyr Phe Thr Arg Lys
117                325                330                335
119 ccc ggc atc ttt ttg gga tgg gcc gat ttg ctg aat tcc aag gac att     1056
120 Pro Gly Ile Phe Leu Gly Trp Ala Asp Leu Leu Asn Ser Lys Asp Ile
121             340                345                350
123 cgt aac tct atg ccc act att ttt gtc gtc gtc atg tgc ttc atg ctg     1104
124 Arg Asn Ser Met Pro Thr Ile Phe Val Val Val Met Cys Phe Met Leu
125          355                360                365
127 ccc gcc aat tat gct ttc cta cgc tac tgc acc aga cgc ggt ggt cca     1152
128 Pro Ala Asn Tyr Ala Phe Leu Arg Tyr Cys Thr Arg Arg Gly Gly Pro
129     370                375                380
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131 gtg ccc acg ggt ccc act cca tcg ctg atc acc tgg aag ttc atc cag    1200
132 Val Pro Thr Gly Pro Thr Pro Ser Leu Ile Thr Trp Lys Phe Ile Gln
133 385             390             395             400
135 acc aag gtg cca tgg ggt ctg gtg ttc ctg ctt ggc ggt ggc ttc gct    1248
136 Thr Lys Val Pro Trp Gly Leu Val Phe Leu Leu Gly Gly Gly Phe Ala
137             405             410             415
139 ttg gcc gaa ggc agc aag cag agc ggc atg gcc aag ctg att ggc aat    1296
140 Leu Ala Glu Gly Ser Lys Gln Ser Gly Met Ala Lys Leu Ile Gly Asn
141             420             425             430
143 gct ctg att gga ttg aag gtt ctg ccc aac tct gtc ctc tta ctg gtg    1344
144 Ala Leu Ile Gly Leu Lys Val Leu Pro Asn Ser Val Leu Leu Leu Val
145         435             440             445
147 gtc atc ctg gtg gct gtg ttc ctg acc gcc ttc agc tcc aat gtg gcg    1392
148 Val Ile Leu Val Ala Val Phe Leu Thr Ala Phe Ser Ser Asn Val Ala
149     450             455             460
151 att gcc aac att att att ccc gtt ctg gcc gag atg tcc ctg gcc att    1440
152 Ile Ala Asn Ile Ile Ile Pro Val Leu Ala Glu Met Ser Leu Ala Ile
153 465             470             475             480
155 gag atc cat cct ctg tac ctg atc ctg ccc gct ggc ttg gcc tgc agt    1488
156 Glu Ile His Pro Leu Tyr Leu Ile Leu Pro Ala Gly Leu Ala Cys Ser
157             485             490             495
159 atg gcc ttc cac ctg ccg gtt agt act ccg ccc aac gct ttg gtt gct    1536
160 Met Ala Phe His Leu Pro Val Ser Thr Pro Pro Asn Ala Leu Val Ala
161             500             505             510
163 ggc tat gcc aac att agg acg aag gac atg gcc att gct gga atc ggt    1584
164 Gly Tyr Ala Asn Ile Arg Thr Lys Asp Met Ala Ile Ala Gly Ile Gly
165         515             520             525
167 ccg acc atc att acc atc atc acc ctg ttt gtt ttc tgc caa acc tgg    1632
168 Pro Thr Ile Ile Thr Ile Ile Thr Leu Phe Val Phe Cys Gln Thr Trp
169     530             535             540
171 ggc ctg gtt gtc tat ccg aac ctt aac tcg ttc ccc gaa tgg gct cag    1680
172 Gly Leu Val Val Tyr Pro Asn Leu Asn Ser Phe Pro Glu Trp Ala Gln
173 545             550             555             560
175 att tat gcc gcg gca gca ctg gga aac aag acg cac tag             1719
176 Ile Tyr Ala Ala Ala Ala Leu Gly Asn Lys Thr His
177             565             570
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181 <211> LENGTH: 572
182 <212> TYPE: PRT
183 <213> ORGANISM: Drosophila melanogaster
185 <400> SEQUENCE: 2
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187 1               5               10              15
188 Asn Phe Phe Ala Asn His Trp Lys Gly Leu Val Val Phe Leu Val Pro
189             20              25              30
190 Leu Leu Cys Leu Pro Val Met Leu Leu Asn Glu Gly Ala Glu Phe Arg
191         35              40              45
192 Cys Met Tyr Leu Leu Leu Val Met Ala Ile Phe Trp Val Thr Glu Ala
193     50              55              60
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194 Leu Pro Leu Tyr Val Thr Ser Met Ile Pro Ile Val Ala Phe Pro Ile
195 65                  70              75                  80
196 Met Gly Ile Met Ser Ser Asp Gln Thr Cys Arg Leu Tyr Phe Lys Asp
197             85                  90                  95
198 Thr Leu Val Met Phe Met Gly Gly Ile Met Val Ala Leu Ala Val Glu
199             100             105             110
200 Tyr Cys Asn Leu His Lys Arg Leu Ala Leu Arg Val Ile Gln Ile Val
201         115             120             125
202 Gly Cys Ser Pro Arg Arg Leu His Phe Gly Leu Ile Met Val Thr Met
203     130             135             140
204 Phe Leu Ser Met Trp Ile Ser Asn Ala Ala Cys Thr Ala Met Met Cys
205 145             150             155             160
206 Pro Ile Ile Gln Ala Val Leu Glu Glu Leu Gln Ala Gln Gly Val Cys
207             165             170             175
208 Lys Ile Asn His Glu Pro Gln Tyr Gln Ile Val Gly Gly Asn Lys Lys
209         180             185             190
210 Asn Asn Glu Asp Glu Pro Pro Tyr Pro Thr Lys Ile Thr Leu Cys Tyr
211         195             200             205
212 Tyr Leu Gly Ile Ala Tyr Ala Ser Ser Leu Gly Gly Cys Gly Thr Ile
213     210             215             220
214 Ile Gly Thr Ala Thr Asn Leu Thr Phe Lys Gly Ile Tyr Glu Ala Arg
215 225             230             235             240
216 Phe Lys Asn Ser Thr Glu Gln Met Asp Phe Pro Thr Phe Met Phe Tyr
217             245             250             255
218 Ser Val Pro Ser Met Leu Val Tyr Thr Leu Leu Thr Phe Val Phe Leu
219             260             265             270
220 Gln Trp His Phe Met Gly Leu Trp Arg Pro Lys Ser Lys Glu Ala Gln
221     275             280             285
222 Glu Val Gln Arg Gly Arg Glu Gly Ala Asp Val Ala Lys Lys Val Ile
223     290             295             300
224 Asp Gln Arg Tyr Lys Asp Leu Gly Pro Met Ser Ile His Glu Ile Gln
225 305             310             315             320
226 Val Met Ile Leu Phe Ile Phe Met Val Val Met Tyr Phe Thr Arg Lys
227             325             330             335
228 Pro Gly Ile Phe Leu Gly Trp Ala Asp Leu Leu Asn Ser Lys Asp Ile
229             340             345             350
230 Arg Asn Ser Met Pro Thr Ile Phe Val Val Val Met Cys Phe Met Leu
231         355             360             365
232 Pro Ala Asn Tyr Ala Phe Leu Arg Tyr Cys Thr Arg Arg Gly Gly Pro
233     370             375             380
234 Val Pro Thr Gly Pro Thr Pro Ser Leu Ile Thr Trp Lys Phe Ile Gln
235 385             390             395             400
236 Thr Lys Val Pro Trp Gly Leu Val Phe Leu Leu Gly Gly Gly Phe Ala
237             405             410             415
238 Leu Ala Glu Gly Ser Lys Gln Ser Gly Met Ala Lys Leu Ile Gly Asn
239             420             425             430
240 Ala Leu Ile Gly Leu Lys Val Leu Pro Asn Ser Val Leu Leu Leu Val
241         435             440             445
242 Val Ile Leu Val Ala Val Phe Leu Thr Ala Phe Ser Ser Asn Val Ala
```

```
243      450                  455                  460
244 Ile Ala Asn Ile Ile Ile Pro Val Leu Ala Glu Met Ser Leu Ala Ile
245 465                  470                  475                  480
246 Glu Ile His Pro Leu Tyr Leu Ile Leu Pro Ala Gly Leu Ala Cys Ser
247                  485                  490                  495
248 Met Ala Phe His Leu Pro Val Ser Thr Pro Pro Asn Ala Leu Val Ala
249                  500                  505                  510
250 Gly Tyr Ala Asn Ile Arg Thr Lys Asp Met Ala Ile Ala Gly Ile Gly
251          515                  520                  525
252 Pro Thr Ile Ile Thr Ile Ile Thr Leu Phe Val Phe Cys Gln Thr Trp
253      530                  535                  540
254 Gly Leu Val Val Tyr Pro Asn Leu Asn Ser Phe Pro Glu Trp Ala Gln
255 545                  550                  555                  560
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257                  565                  570
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260 <211> LENGTH: 562
261 <212> TYPE: PRT
262 <213> ORGANISM: Drosophila melanogaster
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267 Ile Phe His Trp Arg Gly Lys Ala Ser Ile Ile Ile Pro Leu Ile Thr
268              20                  25                  30
269 Leu Pro Ile Leu Ile Tyr Gly Phe Gln Thr Asp Met Ala Glu Phe Lys
270          35                  40                  45
271 Cys Leu Trp Leu Ile Val Thr Met Ala Leu Leu Trp Ile Thr Glu Thr
272      50                  55                  60
273 Leu Pro Ile Tyr Val Thr Ala Leu Phe Pro Leu Val Phe Cys Pro Leu
274 65                  70                  75                  80
275 Leu Gly Leu Val Asn Ala Ser Ile Val Cys Lys Gln Tyr Phe Thr Asp
276                  85                  90                  95
277 Thr Ile Val Val Phe Leu Gly Gly Leu Ile Val Ala Leu Gly Ile Glu
278                  100                 105                 110
279 Tyr Ser Asn Leu His Thr Arg Ile Ala Leu Arg Val Ile Arg Ile Val
280          115                 120                 125
281 Gly Gly Ser Pro Arg Arg Leu Phe Val Gly Leu Met Ser Val Ser Thr
282      130                 135                 140
283 Phe Met Gly Leu Trp Ile Ser Asn Ser Ala Gly Thr Ala Met Met Cys
284 145                 150                 155                 160
285 Pro Ile Val Lys Ala Leu Val Asn Glu Leu Asp Thr Asn Lys Ile Phe
286                  165                 170                 175
287 Pro Val Tyr Met Thr Gln Glu Glu Glu Pro Val Glu Glu Gly Glu Pro
288                  180                 185                 190
289 Pro His Pro Ser Lys Ile Thr Val Ala Phe Tyr Ala Gly Ile Ala Tyr
290          195                 200                 205
291 Ala Ser Ser Ile Gly Gly Leu Gly Thr Leu Ile Gly Thr Gly Thr Asn
292      210                 215                 220
293 Leu Val Phe Arg Gly Ile Tyr Thr Glu Arg Phe Pro Thr Ser Thr Val
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VERIFICATION SUMMARY   DATE: 07/16/2003
PATENT APPLICATION: US/10/017,479A   TIME: 15:45:41

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